

## SEQUENCE LISTING

<110> SmithKline Beecham Biologicals S.A.

<120> Novel Compounds

<130> BM45351

<160> 6

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2169

<212> DNA

<213> *Neisseria meningitidis*

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accgtcggca caaaaatccc cgcttctttg cgcgaaattc cgcaatccgt cagtatcatc	240
accaaccagc aggtcaaaga ccgcaatgtt gatacgtttg accagttggc gcgcaaaacg	300
ccgggcctgc gcgtgttgag caacgatgac ggacgctctt cggtttacgc gcgcgggttac	360
gaatacagcg aatacaacat cgacggcctg cccgcgcaga tgcagagtat caacggcacg	420
ctgcccattc tggttcgcctt cgaccgcgtg gaagtgatgc gcggggccgag cggactgttc	480
gacagcagcg gcgagatggg cggtatcgtg aatctggtgc gcaaacgccc gaccaaagcg	540
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gtatcgggca gcctcaattc agacggcagc gtgcgcggcc gcgtgatggc gcagaccgtc	660
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<211> 722

<212> PRT

<213> *Neisseria meningitidis*

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 Leu Glu Thr Val His Ile Lys Gly Gln Arg Ser Tyr Asn Ala Ile Val  
 35 40 45  
 Thr Glu Lys Asn Gly Asp Tyr Ser Ser Phe Ala Val Thr Val Gly Thr  
 50 55 60  
 Lys Ile Pro Ala Ser Leu Arg Glu Ile Pro Gln Ser Val Ser Ile Ile  
 65 70 75 80  
 Thr Asn Gln Gln Val Lys Asp Arg Asn Val Asp Thr Phe Asp Gln Leu  
 85 90 95  
 Ala Arg Lys Thr Pro Gly Leu Arg Val Leu Ser Asn Asp Asp Gly Arg  
 100 105 110  
 Ser Ser Val Tyr Ala Arg Gly Tyr Glu Tyr Ser Glu Tyr Asn Ile Asp  
 115 120 125  
 Gly Leu Pro Ala Gln Met Gln Ser Ile Asn Gly Thr Leu Pro Asn Leu  
 130 135 140

Phe Ala Phe Asp Arg Val Glu Val Met Arg Gly Pro Ser Gly Leu Phe  
 145 150 155 160  
 Asp Ser Ser Gly Glu Met Gly Gly Ile Val Asn Leu Val Arg Lys Arg  
 165 170 175  
 Pro Thr Lys Ala Phe Gln Gly His Ala Ala Ala Gly Phe Gly Thr His  
 180 185 190  
 Lys Gln Tyr Lys Ala Glu Ala Asp Val Ser Gly Ser Leu Asn Ser Asp  
 195 200 205  
 Gly Ser Val Arg Gly Arg Val Met Ala Gln Thr Val Gly Ala Ser Pro  
 210 215 220  
 Arg Pro Ala Glu Lys Asn Asn Arg His Glu Thr Phe Tyr Ala Ala Ala  
 225 230 235 240  
 Asp Trp Asp Ile Asn Pro Asp Thr Val Leu Gly Ala Gly Tyr Leu Tyr  
 245 250 255  
 Gln Gln Arg His Leu Ala Pro Tyr Asn Gly Leu Pro Ala Asp Ala Asn  
 260 265 270  
 Asn Lys Leu Pro Ser Leu Pro Gln His Val Phe Val Gly Ala Asp Trp  
 275 280 285  
 Asn Lys Phe Lys Met Asn Ser His Asp Val Phe Ala Asp Leu Lys His  
 290 295 300  
 Tyr Phe Gly Asn Gly Gly Tyr Gly Lys Val Gly Met Arg Tyr Ser Asp  
 305 310 315 320  
 Arg Asp Ala Asp Ser Asn Tyr Ala Phe Ala Gly Ser Lys Leu Gly Met  
 325 330 335  
 Lys Thr Pro Ala Gly Arg Pro Gly Cys Asn Thr Ala Asp Asp Lys Ala  
 340 345 350  
 Cys Ala Val Gly Leu Gly Thr Glu Ile Lys Gln Lys Ala Leu Ala Phe  
 355 360 365  
 Asp Ala Ser Tyr Ser Arg Pro Phe Arg Leu Gly Asn Thr Ala Asn Glu  
 370 375 380  
 Phe Val Ile Gly Ala Asp Tyr Asn Arg Phe Arg Ser Thr Asn Glu Gln  
 385 390 395 400  
 Gly Arg Thr Thr Leu Tyr Ala Arg Gly Gly Leu Ala Leu Asn Glu Phe  
 405 410 415  
 Arg Ser Ile Pro Gln Val Asp Leu Ile Ala Asn Ala Arg Lys Gly Val  
 420 425 430  
 Arg Gly Tyr Ser His Thr Val Ala Thr Glu Asn Leu Asp Glu Phe Gly  
 435 440 445  
 Ile Tyr Gly Lys Ser Thr Phe His Pro Ala Asp Gly Leu Ser Leu Ile  
 450 455 460  
 Gly Gly Gly Arg Leu Gly His Tyr Lys Ile Glu Ser Gly Glu Gly Lys

465                      470                      475                      480  
 Thr Leu His Lys Ala Ser Lys Thr Lys Phe Thr Gly Tyr Ala Gly Ala  
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 Val Tyr Asp Leu Asn Asp Asn Asn Ser Leu Tyr Leu Ser Leu Ser Gln  
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 Leu Tyr Thr Pro Gln Thr Asn Leu Asp Ala Asp Gly Lys Leu Leu Lys  
                          515                      520                      525  
 Pro Arg Gln Gly Asn Gln Phe Glu Val Gly Tyr Lys Gly Ser Tyr Met  
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 Asp Asp Arg Leu Asn Ala Arg Val Ser Phe Tyr Arg Met Lys Asp Lys  
 545                      550                      555                      560  
 Asn Ala Ala Ala Pro Leu Asn Pro Asn Asn Lys Lys Thr Arg Tyr Ala  
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 Ala Leu Gly Lys Arg Val Met Glu Gly Val Glu Thr Glu Ile Ser Gly  
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 Ala Val Thr Pro Lys Trp Gln Ile His Ala Gly Tyr Ser Tyr Leu His  
                          595                      600                      605  
 Ser Gln Ile Lys Thr Ala Ser Asn Ser Arg Asp Asp Gly Ile Phe Leu  
                          610                      615                      620  
 Leu Met Pro Lys His Ser Ala Asn Leu Trp Thr Thr Tyr Gln Val Thr  
 625                      630                      635                      640  
 Pro Glu Leu Thr Ile Gly Gly Gly Val Asn Ala Met Ser Gly Ile Thr  
                          645                      650                      655  
 Ser Ser Ala Gly Met His Ala Gly Gly Tyr Ala Thr Phe Asp Ala Met  
                          660                      665                      670  
 Ala Ala Tyr Arg Phe Thr Pro Lys Leu Lys Leu Gln Ile Asn Ala Asp  
                          675                      680                      685  
 Asn Ile Phe Asn Arg His Tyr Tyr Ala Arg Val Gly Gly Ala Asn Thr  
                          690                      695                      700  
 Phe Asn Ile Pro Gly Ser Glu Arg Thr Trp Thr Ala Asn Leu Arg Tyr  
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 Ser Phe

&lt;210&gt; 3

&lt;211&gt; 2078

&lt;212&gt; DNA

<213> *Neisseria meningitidis*

&lt;400&gt; 3

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 cgacaaaca atataaagcc gagggcgacg tatcgggcag cctcaattca gacggcagcg 540  
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<210> 4

<211> 691

<212> PRT

<213> *Neisseria meningitidis*

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 35 40 45  
 Ile Thr Asn Gln Gln Val Lys Asp Arg Asn Val Asp Thr Phe Asp Gln  
 50 55 60  
 Leu Ala Arg Lys Thr Pro Gly Leu Arg Val Leu Ser Asn Asp Asp Gly  
 65 70 75 80  
 Arg Ser Ser Val Tyr Ala Arg Gly Tyr Glu Tyr Ser Glu Tyr Asn Ile  
 85 90 95  
 Asp Gly Leu Pro Ala Gln Met Gln Ser Ile Asn Gly Thr Leu Pro Asn  
 100 105 110  
 Leu Phe Ala Phe Asp Arg Val Glu Val Met Arg Gly Pro Ser Gly Leu  
 115 120 125  
 Phe Asp Ser Ser Gly Glu Met Gly Gly Ile Val Asn Leu Val Arg Lys  
 130 135 140  
 Arg Pro Thr Lys Ala Phe Gln Gly His Ala Ala Ala Gly Phe Gly Thr  
 145 150 155 160  
 His Lys Gln Tyr Lys Ala Glu Ala Asp Val Ser Gly Ser Leu Asn Ser  
 165 170 175  
 Asp Gly Ser Val Arg Gly Arg Val Met Ala Gln Thr Val Gly Ala Ser  
 180 185 190  
 Pro Arg Pro Ala Glu Lys Asn Asn Arg His Glu Thr Phe Tyr Ala Ala  
 195 200 205  
 Ala Asp Trp Asp Ile Asn Pro Asp Thr Val Leu Gly Ala Gly Tyr Leu  
 210 215 220  
 Tyr Gln Gln Arg His Leu Ala Pro Tyr Asn Gly Leu Pro Ala Asp Ala  
 225 230 235 240  
 Asn Asn Lys Leu Pro Ser Leu Pro Gln His Val Phe Val Gly Ala Asp  
 245 250 255  
 Trp Asn Lys Phe Lys Met Asn Ser His Asp Val Phe Ala Asp Leu Lys  
 260 265 270  
 His Tyr Phe Gly Asn Gly Gly Tyr Gly Lys Val Gly Met Arg Tyr Ser  
 275 280 285  
 Asp Arg Asp Ala Asp Ser Asn Tyr Ala Phe Ala Gly Ser Lys Leu Gly  
 290 295 300  
 Met Lys Thr Pro Ala Gly Arg Pro Gly Cys Asn Thr Ala Asp Asp Lys  
 305 310 315 320  
 Ala Cys Ala Val Gly Leu Gly Thr Glu Ile Lys Gln Lys Ala Leu Ala

325 330 335  
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 340 345 350  
 Glu Phe Val Ile Gly Ala Asp Tyr Asn Arg Phe Arg Ser Thr Asn Glu  
 355 360 365  
 Gln Gly Arg Thr Thr Leu Tyr Ala Arg Gly Gly Leu Ala Leu Asn Glu  
 370 375 380  
 Phe Arg Ser Ile Pro Gln Val Asp Leu Ile Ala Asn Ala Arg Lys Gly  
 385 390 395 400  
 Val Arg Gly Tyr Ser His Thr Val Ala Thr Glu Asn Leu Asp Glu Phe  
 405 410 415  
 Gly Ile Tyr Gly Lys Ser Thr Phe His Pro Ala Asp Gly Leu Ser Leu  
 420 425 430  
 Ile Gly Gly Gly Arg Leu Gly His Tyr Lys Ile Glu Ser Gly Glu Gly  
 435 440 445  
 Lys Thr Leu His Lys Ala Ser Lys Thr Lys Phe Thr Gly Tyr Ala Gly  
 450 455 460  
 Ala Val Tyr Asp Leu Asn Asp Asn Asn Ser Leu Tyr Leu Ser Leu Ser  
 465 470 475 480  
 Gln Leu Tyr Thr Pro Gln Thr Asn Leu Asp Ala Asp Gly Lys Leu Leu  
 485 490 495  
 Lys Pro Arg Gln Gly Asn Gln Phe Glu Val Gly Tyr Lys Gly Ser Tyr  
 500 505 510  
 Met Asp Asp Arg Leu Asn Ala Arg Val Ser Phe Tyr Arg Met Lys Asp  
 515 520 525  
 Lys Asn Ala Ala Ala Pro Leu Asn Pro Asn Asn Lys Lys Thr Arg Tyr  
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 Ala Ala Leu Gly Lys Arg Val Met Glu Gly Val Glu Thr Glu Ile Ser  
 545 550 555 560  
 Gly Ala Val Thr Pro Lys Trp Gln Ile His Ala Gly Tyr Ser Tyr Leu  
 565 570 575  
 His Ser Gln Ile Lys Thr Ala Ser Asn Ser Arg Asp Asp Gly Ile Phe  
 580 585 590  
 Leu Leu Met Pro Lys His Ser Ala Asn Leu Trp Thr Thr Tyr Gln Val  
 595 600 605  
 Thr Pro Glu Leu Thr Ile Gly Gly Gly Val Asn Ala Met Ser Gly Ile  
 610 615 620  
 Thr Ser Ser Ala Gly Met His Ala Gly Gly Tyr Ala Thr Phe Asp Ala  
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 Met Ala Ala Tyr Arg Phe Thr Pro Lys Leu Lys Leu Gln Ile Asn Ala  
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Asp Asn Ile Phe Asn Arg His Tyr Tyr Ala Arg Val Gly Gly Ala Asn  
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Tyr Ser Phe  
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30

<210> 6  
<211> 33  
<212> DNA  
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33